IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Stuart A. Lipton
Serial No. : 08/346,910
Filed : November 30, 1994
Title : PROTEIN 68075 AND ITS USE FOR REGENERATING NERVE CELL PROCESSES

Art Unit : 1647
Examiner : Gucker, S.

BOX AF
Commissioner for Patents
Washington, D.C. 20231

BRIEF ON APPEAL

(1) Real Party in Interest

The inventor, Stuart A. Lipton, is the owner of this patent application and the real party in interest in this appeal.

(2) Related Appeals and Interferences

There are no related appeals or interferences.

(3) Status of Claims

Claims 8, 11, and 12 are allowed.

This appeal is taken from the final rejection of claim 14.

No other claims are pending in this application.

(4) Status of Amendments

The claims under consideration in the final rejection mailed November 21, 2000 (paper 25, "the Final Rejection") have not been amended.

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I hereby certify under 37 CFR §1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, Washington, D.C. 20231.

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(5) Summary of Invention

Applicant has invented isolated nucleic acids from a human gene involved in neuronal differentiation, later termed MEF2C. Claim 14 focuses on one of these clone, which was deposited with the American Type Tissue Collection using U.S. Patent and Trademark Office approved procedures, and designated ATCC 97525.

(6) Issues

A) Does The Specification As Filed, Which Discloses Five Clones, Including ATTC 97525, Demonstrate To Those Skilled In The Field That The Applicant Was In Possession Of The Invention Featured In Claim 14, As Required By 35 U.S.C. §112 ¶1?

B) Does The Specification As Filed, Which Discloses Five Clones Including ATTC 97525, Enable Those Skilled In The Field To Practice The Invention Featured In Claim 14, As Required By 35 U.S.C. §112 ¶1?

(7) Grouping of Claims

Only one claim is at issue in this appeal, claim 14. The remaining pending claims stand allowed.

(8) Argument

Claim 14 stands rejected under 35 U.S.C. §112 ¶1 on the finding that the specification as filed lacks a written description of the invention of claim 14 (this rejection appears in paragraphs 4 and 6 of the Final Rejection) and the specification as filed fails to enable those skilled in the field at the time of the invention to make, use and practice the invention of claim 14 (this rejection appears in paragraph 5 of the Final Rejection).

A. The Specification As Filed, Which Discloses Five Clones, Including ATTC 97525, Demonstrates That The Applicant Was In Possession Of The Invention Featured In Claim 14 as required by 35 USC §112 ¶1.

The statutory requirement to provide a written description the invention is embodied in 35 U.S.C. §112 ¶1, "The specification shall contain a written description of the invention . . .." This statutory requirement has long been interpreted by the courts as requiring that the specification demonstrate to one skilled in the art to which the invention pertains that the inventor had possession of the claimed invention at the time of filing the patent application. See e.g., *Regents of California v. Eli Lilly & Co.*, 119F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997), hereinafter *Eli Lilly*.

Despite the clear patentability of biotechnological inventions, in the early days of biotechnology such inventions presented a particular challenge to the courts: how does one adequately describe or enable an invention going to the essence of life itself? Faced with this problem, the Court of Customs and Patent Appeals, predecessor to the Court of Appeals for the Federal Circuit, held that, where a patent specification discloses biological material that has been deposited with a recognized public depository and is subject to specified maintenance procedures, the deposit of such material at some time prior to issue of the patent is sufficient to satisfy both the written description and enablement requirements of 35 USC §112¶1 for inventions drawn to either the material itself (i.e., a cell line), or of products made by that cell line (e.g., antibiotics). See e.g., *In re Aroguodelis, De Boer, Eble and Herr*, 168 USPQ 99 (CCPA 1970).

In the present case the Examiner has allowed claims 8, 11 and 12, drawn to nucleic acids comprising deposited clones ATCC 68075, ATTC 75949, and ATTC 97525. The deposit of these clones are described in the specification as filed, although the accession numbers of the latter two clones were assigned by the depository after the present application was filed, as permitted pursuant to *In re Lundak*, 773 F.2d 1216, 227 USPQ 90 (Fed. Cir. 1983). Thus, the issue is clearly not whether the deposited clones were was adequately described in the specification, since the Examiner has agreed they were so described, but whether isolated nucleic acid fragments of at least 20 continuous nucleotides were adequately described in the specification in support of claim 14, the only claim that remains rejected.

So there is no question that MEF2C clone ATCC 97525 is described. Nor is there any question of Applicant's possession of fragments of at least 15-20 continuous bases of the nucleic acid of a clone that encoding human a large portion of the MEF2C gene. See page 4, lines 10-20 of the specification. There can be no question, then, that claim 14 is fully supported by the specification as filed. So the specification evidences a clear invention of each and every fragment of 20 or more nucleotides.

The Final Rejection on appeal discusses the written description ("failure-to-demonstrate-possession") rejection in paragraphs 4 and 6. The rationale for the rejection in paragraph 6 is that the claim includes nucleic acids of non-human species. Presumably the Examiner relies on the holding of the Court of Appeals for the Federal Circuit that a generic statement, such as the term "mammalian insulin cDNA" is not, without more, an adequate written description of an invention claiming the nucleotide sequence for human insulin. *Eli Lilly,* 43 USPQ2d 1398. Thus, the *Lilly* court stated, "[t]he description requirement of the patent statute requires a description of an invention, not an indication of a result that one might achieve if one made that invention." *Id.* at 1406.

The Lilly court did not institute a per se rule banning claims that cover DNA from multiple species. Instead, the *Eli Lilly* court took care to indicate that structural information about the claimed genus was different in kind from a mere desired result. The court indicated that, in claims involving chemical materials such as proteins and polynucleotides,

> "generic formulae usually indicate with specificity what the generic claims encompass. One skilled in the art can distinguish such a formula from others and can identify many of the species that the claims encompass. Accordingly, such a formula is usually an adequate description of the claimed genus." *Id.*

Claim 14 of the current application is drawn to isolated nucleic acids of a defined structure – i.e., containing 20-mers of a specified clone (clone 97525) which has been properly deposited and thus it is a far cry from the "desirable result" or "functional" claim that troubled the *Eli Lilly* court. If *Eli Lilly* doesn't actually support patentability, it most certainly provides no basis for this aspect of the rejection, and the Examiner's complaints about coverage of DNA from different species simply lacks legal support.

The Examiner also complains about the number of fragments covered in claim 14.

The number of nucleic acid species encompassed by claim 14 does not obviate the Applicant' clear compliance with the written description requirement, any more than if the claims were drawn to a large number of chemical compounds defined by a generic chemical structure having conventional "R" groups. The latter claim type is found in many, if not most, issued US patents claiming non-DNA, non-protein chemical compounds.

The specification, including deposited clone 97525, provides a written disclosure of the chemical entities claimed. Each and every nucleic acid consisting of at least 20 contiguous nucleotides of the disclosed clone can be determined by this disclosure; thus isolated nucleic acids comprising such structures can be readily identified Preparing an exhaustive listing of such 20-mers might be somewhat laborious if done by hand (or might be done using a computer otherwise) but such labor does not destroy patentability. The *PTO Final Examiner Guidelines on Written Description Requirement*, 61 BNA Patent, Trademark & Copyright Journal 269 (Jan. 12, 2001), says

> "if an applicant disclosed an amino acid sequence, it would be unnecessary to provide an explicit disclosure of nucleic acid sequences that encoded the amino acid sequences [despite the redundancy of the genetic code and the resulting large number of such nucleotide sequences, because] a disclosure of an amino acid sequence would provide sufficient information such that one would accept that the applicant was in possession of the full genus of nucleic acids encoding" such amino acid sequence. *Id.* at 280, footnote 57.

Similarly, the person of skill in the art would readily accept that the present Applicants were in possession of the isolated nucleic acids of claim 14.

It is worth noting that the Examiner has not and could not challenge the utility of the claimed invention. Pages 3 and 4 of the specification clearly show that the claimed isolated nucleic acids have a credible utility as selective probes in preliminary screens of nucleic acids encoding MEF2C and related proteins. From the small pool of clones homologous to the claimed nucleic acids, the specification discloses that the MEF2C-encoding clones "can be identified by standard procedures"; such procedures include nucleic acid sequencing, the use of multiple probes, and activity assays.

Finally, in paragraph 4 of the Final Rejection on appeal, the Examiner supported the written description rejection with a "new matter" analysis, although there is no rejection under 35 U.S.C. §132.

> [A] Fair reading of the specification indicates that the Applicant does not have either verbatim or conceptual support for the recited limitation of a nucleic acid that would selectively hybridize to nucleic acid encoding human MEF2C (emphasis in original).

In support of this position the Examiner has quoted the specification at page 4, lines 13-20:

> [T]he probe is a portion of at least 15-20 contiguous bases of the nucleic acid encoding human 68075 [this protein is now called MEF2C]. This probe nucleic acid is used under standard stringent hybridization conditions to identify nucleic acid homologous to that encoding the human 68075. Not all such homologous sequences will encode a 68075 protein but those which do can be identified bv standard procedures. (emphasis added by Examiner).

The Examiner has taken the position that this passage does not support (and in fact contradicts) disclosure of the claimed isolated nucleic acids that selectively hybridize to human MEF2C nucleic acids. This position is erroneous for the following reasons.

As an initial matter, Applicant respectfully contends the Examiner has failed to consider the claim as a whole. Instead he has set up a "straw man" by improperly interpreting the claim and then rejecting the claim as so interpreted.

Claim 14 contains both structural and functional limitations. The claim is drawn to a nucleic acid fragment comprising a sequence of 20 or more contiguous nucleotides of clone ATTC 97525. This is a wholly structural limitation, albeit one that encompasses a genus of compounds. As discussed above, it is clear that the chemical structure of this genus of compounds is properly described by the specification, which includes the deposited clone ATTC 97525.

The additional limitation of claim 14, that such fragments selectively hybridize to human MEF2C nucleic acid, is a functional limitation. The Examiner's rejection focuses on this language and is based on the fact, as stated in the quotation from the specification cited above, that some nucleic acid fragments within the claim's structural limitations

will not hybridize solely MEF2C nucleic acid, but may hybridize to other structurally related nucleic acids. Based on that fact, the examiner, in effect, reads the phrase "selectively hybridize" as meaning "hybridize to the complete exclusion of other hybridization" i.e., 100% specific hybridization.

The word "selective" is defined as "judicious or restrictive in a choice." *Webster's New American Dictionary* 471 (Marrian-Webster 1995). Applicant has not defined the word otherwise in the specification; thus, the claim term "selectively hybridize" must be construed to mean that the use of a probe that: a) meets the above described structural limitations; and b) hybridizes to nucleic acids in a manner that reduces the number of possible hybridizing nucleic acids to a subset which includes MEF2C.

Contrary to the clear meaning of the claim, the Examiner's comments imply that he understands "selective" to have a very narrow meaning that is a specialized meaning of the word "specific". i.e., "having a **unique** effect or influence or reacting in only one way or with only one thing." *Id.* at 497. There is simply no support for this unusual interpretation of the word "selective". Even if Applicant had used the related word "specific", the ordinary meaning of that word does not require that the activity be "unique". For example, when specificity is used to describe bioassays, it is used in its relative sense as an indication of the possibility (statistically) of false positives. So the Examiner has changed the claim wording from "selective" to "specific", and then he has gone further to adopt a very specialized meaning of the word specific. There is no basis for this claim interpretation.

Claim 14 requires that the claimed fragments be able to discriminate MEF2C nucleic acids from at least some other nucleic acids, but not necessarily all such nucleic acids with 100% accuracy.

The functional terms of claim 14 now being properly construed, it can be seen that the present specification provides able description of the selectivity of the claimed nucleic acid fragments. First, the quoted passage from the specification, far from contradicting the functional claim limitation, actually supports it, as it clearly indicates that the use of the claimed probes is useful as a means to obtain a small pool of nucleic

acids from which MEF2C-encoding nucleic acids can be specifically identified using additional steps and standard procedures, such as nucleic acid sequencing.

Also, the specification provides working examples of the use of nucleic acid fragments comprising the MEF2C coding sequence (identified as TR1, TR2A, TR2B (clone 97525), TR3A, TR3B and TR3C on page 8) and TR2B at least has exactly the properties contained in the limitations of claim 14. This aspect of the specification is therefore independent (and independently sufficient) written description supporting claim 14.

For all of these reasons, and with due respect to the Examiner, claim 14 clearly meets the written description requirement of 35 USC 112¶ 1, and Applicant requests that the Board of Patent Appeals and Interferences decide Issue A in the affirmative, reversing the Examiner's rejection of claim 14 as lacking adequate written description in the specification pursuant to 35 USC 112¶1.

B. The Specification as Filed Enables Claim 14.

In the Office Action mailed November 11, 2000 the Examiner rejected claim 14, stating that the specification does not describe how to make and use the invention claimed therein as required by 35 USC 112¶1. The Applicant respectfully disagrees, and maintains that the person of ordinary skill in the art, both at the priority date of this patent application, and today, would be able to make and use the present invention without undue experimentation in light of the specification land the general knowledge of one of skill in the art.

The Examiner's rationale alleging lack of enablement is similar to that presented above for the written description rejection:

> As set forth in ¶4 above, the specification discloses that probes of at least 20 bases cannot selectively hybridize to nucleic acid encoding human MEF2C because not all such sequences which the probe will hybridize to will actually encode human MEF2C, i. e. the hybridization is not selective because other standard procedures for identification must be performed. Therefore, a probe that meets the limitation of selective hybridization to an encoding nucleic acid sequence has not been taught by the disclosure. The specification provides no

written description, no working examples, and no specific or substantial guidance as to how the skilled artisan could routinely make and use fragments of nucleic acid comprising at least 20 contiguous bases of clone ATCC 97525 wherein said nucleic acid is able to selectively hybridize to nucleic acid encoding human MEF2C because the instant disclosure admits that such nucleic acid fragments will hybridize nonselectively to nucleic acid that does not encode human MEF2C.

Office Action mailed November 11, 2000 at pages 3 and 4.

The appellant respectfully contends that the basis for this rejection is erroneous both in fact and in law.

Under the enablement requirement of 35 USC §112¶1, a patent specification must disclose to those of skill in the art to which the invention pertains how to make and use the claimed invention. See e.g., *Johns Hopkins University v. Cellpro Inc.*, 47 USPQ2d 1705 (Fed. Cir. 1998); *In re Wands,* 858 F.2d 1400, 8 USPQ2d 1217 (Fed. Cir. 1988). Contrary to the Examiner's contention, and as explained above, the appellant has provided and deposited examples of the claimed nucleic acid fragments and working examples showing their use as selective probes of MEF2C nucleic acids. Moreover, the specification gives detailed information on the construction of these clones. Finally, clone ATTC 97525, to which claim 14 refers, has been deposited and is effectively incorporated as part of the specification.

The Examiner's argument allegedly justifying the lack of enablement rejection of claim 14, like the rationale for the written description rejection, appears to be based on a misunderstanding of the claim term "selectively hybridize." As explained above, the claimed nucleic acid fragments are useful as probes for the identification of MEF2C nucleic acids. The mere fact that they are not all necessarily specific for MEF2C nucleic acid acids, and that the unique identification of MEF2C nucleic acids may require one or more additional steps does not obviate the actual, credible utility of the claimed nucleic acids, as demonstrated in the specification.

The Examiner has not disputed that the specification enables those of skill in the art how to make the invention of claim 14. Thus, the only issue is whether their use is taught. As indicated above, the specification teaches one of skill in the art all they would have to know to make use of the nucleic acid fragments as a tool for the identification of

nucleic acids encoding the MEF2C protein. The fact that some nucleic acids not encoding MEF2C might also be identified using the claimed fragments is immaterial; at the priority date the art had no difficulty sorting positive results from negative results using well known techniques including nucleic acid sequencing and the use of multiple probes. See also Sambrook et al., *Molecular Cloning: A Laboratory Manual* (2d ed. Cold Spring Harbor Laboratory Press 1989).

For this reason, Appellant respectfully requests that the Board of Patent Appeals and Interferences decide Issue B in the affirmative, and reverse the Examiner's rejection of claim 14 as lacking enabling support in the specification.

The brief fee of $155 is enclosed. Please apply any other charges or credits to Deposit Account No. 06-1050.

Respectfully submitted,

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Appendix

The pending claims are claims 8, 11, 12 and 14. Only claim 14 is at issue in this appeal.

8. An isolated nucleic acid comprising Clone ATCC 97525.

11. An isolated nucleic acid comprising Clone ATCC 68075.

12. An isolated nucleic acid comprising Clone ATCC 75949.

14. An isolated fragment of nucleic acid comprising at least 20 contiguous bases of clone ATCC 97525, wherein said nucleic acid is able to selectively hybridize to nucleic acid encoding human MEF2C.